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Reviewer: markspencer

Timestamp: [year=2008; month=10; day=29; hr=16; min=1; sec=49; ms=627; ]

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Application No: 09622646 Version No: 2.0

**Input Set:****Output Set:**

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**Finished:** 2008-09-24 11:29:49.847  
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**Total Warnings:** 27  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 31  
**Actual SeqID Count:** 31

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**Input Set:**

**Output Set:**

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**No. of SeqIDs Defined:** 31  
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Error code

Error Description

This error has occurred more than 20 times, will not be displayed

# SEQUENCE LISTING

<110> OZAKI, YASUKO  
KOISHIHARA, YASUO

<120> IMMUNOCHEMICAL ASSAY FOR ANTI-HM1.24 ANTIBODY

<130> 053466-0286

<140> 09622646

<141> 2000-08-21

<150> PCT/JP99/00885

<151> 1999-02-25

<150> JP 10-60613

<151> 1998-02-25

<160> 31

<170> PatentIn Ver. 3.5

<210> 1

<211> 399

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(396)

<220>

<223> Nucleotide sequence of extracellular domain  
of soluble HM 1.24 antigenic protein

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Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg	
1 5 10 15	

aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag ggc	96
Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly	
20 25 30	

ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg atg	144
Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met	
35 40 45	

gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag aaa	192
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys	
50 55 60	

gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt cag	240
Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln	
65 70 75 80	

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gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc tta 288
Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
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agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc cag gac tcc 336
Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
      100             105             110

agc tcc gct gcg gcg ccc cag ctg ctg att gtg ctg ctg ggc ctc agc 384
Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
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gct ctg ctg cag tga 399
Ala Leu Leu Gln
      130

<210> 2
<211> 510
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nucleotide
      sequence coding for a fusion protein comprising
      leader sequence, FLAG peptide and soluble HM 1.24
      antigenic protein

<220>
<221> CDS
<222> (12)..(494)

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      Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr
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gct aca ggt gtc cac tcc gac tac aaa gac gat gac gat aaa ggt acc 98
Ala Thr Gly Val His Ser Asp Tyr Lys Asp Asp Asp Asp Lys Gly Thr
      15             20             25

aac agc gag gcc tgc cgg gac ggc ctt cgg gca gtg atg gag tgt cgc 146
Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
      30             35             40             45

aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag ggc 194
Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
      50             55             60

ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg atg 242
Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
      65             70             75

gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag aaa 290
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
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gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt cag 338
Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
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gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc tta 386
Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
110              115              120              125

agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc cag gac tcc 434
Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
    130              135              140

agc tcc gct gcg gcg ccc cag ctg ctg att gtg ctg ctg ggc ctc agc 482
Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
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Ala Leu Leu Gln
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<210> 3
<211> 445
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nucleotide
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      peptide and soluble HM 1.24 antigenic protein

<220>
<221> CDS
<222> (1)..(429)

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Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
    1              5              10              15

cgg gac ggc ctt cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc 96
Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
    20              25              30

ctg caa caa gag ctg acc gag gcc cag aag ggc ttt cag gat gtg gag 144
Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu
    35              40              45

gcc cag gcc gcc acc tgc aac cac act gtg atg gcc cta atg gct tcc 192
Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser
    50              55              60

ctg gat gca gag aag gcc caa gga caa aag aaa gtg gag gag ctt gag 240
Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu
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gga gag atc act aca tta aac cat aag ctt cag gac gcg tct gca gag 288

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Gly	Glu	Ile	Thr	Thr	Leu	Asn	His	Lys	Leu	Gln	Asp	Ala	Ser	Ala	Glu		
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Val	Glu	Arg	Leu	Arg	Arg	Glu	Asn	Gln	Val	Leu	Ser	Val	Arg	Ile	Ala		
			100					105					110				
gac	aag	aag	tac	tac	ccc	agc	tcc	cag	gac	tcc	agc	tcc	gct	gcg	gcg	384	
Asp	Lys	Lys	Tyr	Tyr	Pro	Ser	Ser	Gln	Asp	Ser	Ser	Ser	Ala	Ala	Ala		
			115					120					125				
ccc	cag	ctg	ctg	att	gtg	ctg	ctg	ggc	ctc	agc	gct	ctg	ctg	cag		429	
Pro	Gln	Leu	Leu	Ile	Val	Leu	Leu	Gly	Leu	Ser	Ala	Leu	Leu	Gln			
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<213> Artificial Sequence																	
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<223> Description of Artificial Sequence: Nucleotide																	
sequence coding for a fusion protein comprising HA																	
peptide and C-terminal-lacking soluble HM 1.24																	
antigenic protein																	
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<221> CDS																	
<222> (1)..(378)																	
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			1			5			10					15			
cgg	gac	ggc	ctt	cgg	gca	gtg	atg	gag	tgt	cgc	aat	gtc	acc	cat	ctc	96	
Arg	Asp	Gly	Leu	Arg	Ala	Val	Met	Glu	Cys	Arg	Asn	Val	Thr	His	Leu		
			20					25				30					
ctg	caa	caa	gag	ctg	acc	gag	gcc	cag	aag	ggc	ttt	cag	gat	gtg	gag	144	
Leu	Gln	Gln	Glu	Leu	Thr	Glu	Ala	Gln	Lys	Gly	Phe	Gln	Asp	Val	Glu		
			35					40				45					
gcc	cag	gcc	gcc	acc	tgc	aac	cac	act	gtg	atg	gcc	cta	atg	gct	tcc	192	
Ala	Gln	Ala	Ala	Thr	Cys	Asn	His	Thr	Val	Met	Ala	Leu	Met	Ala	Ser		
			50				55				60						
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Leu	Asp	Ala	Glu	Lys	Ala	Gln	Gly	Gln	Lys	Lys	Val	Glu	Glu	Leu	Glu		
			65			70			75			80					
gga	gag	atc	act	aca	tta	aac	cat	aag	ctt	cag	gac	gcg	tct	gca	gag	288	
Gly	Glu	Ile	Thr	Thr	Leu	Asn	His	Lys	Leu	Gln	Asp	Ala	Ser	Ala	Glu		
			85					90					95				

gtg gag cga ctg aga aga gaa aac cag gtc tta agc gtg aga atc gcg 336  
 Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala  
 100 105 110

gac aag aag tac tac ccc agc tcc cag gac tcc agc tcc gct tgaggatcc 387  
 Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala  
 115 120 125

<210> 5

<211> 85

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide  
 sequence coding for HA peptide

<220>

<221> CDS

<222> (28)..(54)

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 Tyr Pro Tyr Asp Val Pro Asp Tyr  
 1 5

gct ggtacca aggtggaaat caaacgtacg gaat 85  
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<210> 6

<211> 535

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide  
 sequence coding for CG M/HA-HM164

<220>

<221> CDS

<222> (13)..(453)

<400> 6

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 Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu  
 1 5 10

tgg ctc cca ggt gca cga tgt gca tac cca tac gac gtc cca gac tac 99  
 Trp Leu Pro Gly Ala Arg Cys Ala Tyr Pro Tyr Asp Val Pro Asp Tyr  
 15 20 25

gct ggt acc aac agc gag gcc tgc cgg gac ggc ctt cgg gca gtg atg 147  
 Ala Gly Thr Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met  
 30 35 40 45



gag tgt cgc aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc	195
Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala	
50 55 60	

cag aag ggc ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac	243
Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His	
65 70 75	

act gtg atg gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga	291
Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly	
80 85 90	

caa aag aaa gtg gag gag ctt gag gga gag atc act aca tta aac cat	339
Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His	
95 100 105	

aag ctt cag gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac	387
Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn	
110 115 120 125	

cag gtc tta agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc	435
Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser	
130 135 140	

cag gac tcc agc tcc gct tgaggatcct atgggttacca actacctaga	483
Gln Asp Ser Ser Ser Ala	
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ctggattcgt gacaacatgc ggccgtgata tctacgtatg atcagcctcg ac	535
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

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ggccgcatgt tgtcacgaat	20

<210> 8  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 8	
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<210> 9  
 <211> 27  
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       comprising leader sequence and FLAG coding  
       sequence  
  
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 <210> 13  
 <211> 106

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic DNA  
 comprising leader sequence and FLAG coding  
 sequence

<400> 13  
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<210> 14  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic DNA  
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<400> 14  
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<210> 15  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic DNA  
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<210> 16  
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 <213> Homo sapiens

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 <222> (23)..(562)

<220>  
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 protein expressed on cell membrane

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Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile	
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Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu Ile	
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Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg	
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Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu Leu	
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acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gcc gcc acc	292
Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala Thr	
75 80 85 90	
tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag aag	340
Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu Lys	
95 100 105	
gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act aca	388
Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr Thr	
110 115 120	
tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg aga	436
Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu Arg	
125 130 135	
aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac tac	484
Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr	
140 145 150	
ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg att	532
Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile	
155 160 165 170	
gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc	582
Val Leu Leu Gly Leu Ser Ala Leu Leu Gln	
175 180	
acatcttggga aggtccgtcc tgctcggtt ttcgcttgaa cattcccttg atctcatcag	642
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gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg	762
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tcccacccctg agattgggca tgggggtgcgg tgtggggggc atgtgctgcc tgttggtatg	882
gggtttttttt gggggggggg ttgctttttt ctgggggtctt tgagctccaa aaaaataaac	942
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gggcggccgc ca

1014

<210> 17

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide  
sequence coding for L chain V region version a of  
humanized anti-HM 1.24 antibody

<220>

<221> CDS

<222> (1)..(378)

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